

M. DiBRINO
#15 SK
8/10/00

RECEIVED Page 1 of 7

AUG 10 2000

TECH CENTER 1600/2900 1644

RAW SEQUENCE LISTING DATE: 08/03/2000
PATENT APPLICATION: US/09/019,441 TIME: 12:07:00

Input Set : A:\012712-502.app
Output Set: N:\CRF3\08032000\I019441.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: REFF, Mitchell E.
7 KLOETZER, William S.
8 NAKAMURA, Takehiko
10 (ii) TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
11 ANTIBODIES AND USE THEREOF AS THERAPEUTICS
13 (iii) NUMBER OF SEQUENCES: 35
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
17 (B) STREET: P.O. Box 1404
18 (C) CITY: Alexandria
19 (D) STATE: Virginia
20 (E) COUNTRY: United States
21 (F) ZIP: 22313-1404
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/019,441
C--> 31 (B) FILING DATE: 05-Feb-1998
32 (C) CLASSIFICATION:
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: US 08/803,085
36 (B) FILING DATE: 20-FEB-1997
38 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: Teskin, Robin L.
40 (B) REGISTRATION NUMBER: 35,030
41 (C) REFERENCE/DOCKET NUMBER: 012712-502
43 (ix) TELECOMMUNICATION INFORMATION:
44 (A) TELEPHONE: (703) 836-6620
45 (B) TELEFAX: (703) 836-2021
48 (2) INFORMATION FOR SEQ ID NO: 1:
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 390 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
56 (ii) MOLECULE TYPE: DNA (genomic)
58 (ix) FEATURE:
59 (A) NAME/KEY: CDS
60 (B) LOCATION: 1..390
62 (ix) FEATURE:
63 (A) NAME/KEY: mat_peptide
64 (B) LOCATION: 58..390

RECEIVED

AUG 10 2000

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/019,441

DATE: 08/03/2000

TIME: 12:07:00

Input Set : A:\012712-502.app

Output Set: N:\CRF3\08032000\I019441.raw

```

67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 ATG GCC TGG ACT CTG CTC CTC GTC ACC CTC CTC ACT CAG GGC ACA GGA      48
70 Met Ala Trp Thr Leu Leu Val Thr Leu Leu Thr Gln Gly Thr Gly
71 -19      -15      -10      -5
73 TCC TGG GCT CAG TCT GCC CCG ACT CAG CCT CCC TCT GTG TCT GGG TCT      96
74 Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser
75      -1      1      5      10
77 CCT GGA CAG TCG GTC ACC ATC TCC TGC ACT GGA ACC AGC GAT GAC GTT      144
78 Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val
79      15      20      25
81 GGT GGT TAT AAC TAT GTC TCC TGG TAC CAA CAC CAC CCA GGC AAA GCC      192
82 Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala
83 30      35      40      45
85 CCC AAA CTC ATG ATT TAT GAT GTC GCT AAG CGG GCC TCA GGG GTC TCT      240
86 Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser
87      50      55      60
89 GAT CGC TTC TCT GGC TCC AAG TCT GGC AAC ACG GCC TCC CTG ACC ATC      288
90 Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
91      65      70      75
93 TCT GGG CTC CAG GCT GAG GAC GAG GCT GAT TAT TAC TGT TGT TCA TAT      336
94 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
95      80      85      90
97 ACA ACC AGT AGC ACT TTG TTA TTC GGA AGA GGG ACC CGG TTG ACC GTC      384
98 Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val
99      95      100      105
101 CTA GGT      390
102 Leu Gly
103 110
106 (2) INFORMATION FOR SEQ ID NO: 2:
108      (i) SEQUENCE CHARACTERISTICS:
109          (A) LENGTH: 423 base pairs
110          (B) TYPE: nucleic acid
111          (C) STRANDEDNESS: single
112          (D) TOPOLOGY: linear
114      (ii) MOLECULE TYPE: DNA (genomic)
117      (ix) FEATURE:
118          (A) NAME/KEY: CDS
119          (B) LOCATION: 1..423
121      (ix) FEATURE:
122          (A) NAME/KEY: mat_peptide
123          (B) LOCATION: 58..423
126      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
128 ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG      48
129 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
130 -19      -15      -10      -5
132 GTC CTG TCC CAG CTG CAG CTG CAG GAG TCG GGC CCA GGA GTG GTG AAG      96
133 Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys
134      -1      1      5      10
136 CCT TCG GAG ACC CTG TCC CTC ACC TGC GCT GTC TCT GGT GGC TCT GTC      144

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/019,441
 DATE: 08/03/2000
 TIME: 12:07:00

Input Set : A:\012712-502.app
 Output Set: N:\CRF3\08032000\I019441.raw

```

137 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val
138      15      20      25
140 AGC AGT AGT AAC TGG TGG ACC TGG ATC CGC CAG CCC CCA GGG AAG GGA      192
141 Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly
142 30      35      40      45
144 CTG GAG TGG ATT GGA CGT ATC TCT GGT AGT GGT GGG GCC ACC AAC TAC      240
145 Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr
146      50      55      60
148 AAC CCG TCC CTC AAG AGT CGA GTC ATC ATT TCA CAA GAC ACG TCC AAG      288
149 Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys
150      65      70      75
152 AAC CAG TTC TCC CTG AAC CTG AAC TCT GTG ACC GCC GCG GAC ACG GCC      336
153 Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala
154      80      85      90
156 GTG TAT TAC TGT GCC AGA GAT TGG GCC CAA ATA GCT GGA ACA ACG CTA      384
157 Val Tyr Trp Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu
158      95      100      105
160 GGC TTC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA      423
161 Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser
162 110      115      120
165 (2) INFORMATION FOR SEQ ID NO: 3:
167 (i) SEQUENCE CHARACTERISTICS:
168 (A) LENGTH: 387 base pairs
169 (B) TYPE: nucleic acid
170 (C) STRANDEDNESS: single
171 (D) TOPOLOGY: linear
173 (ii) MOLECULE TYPE: DNA (genomic)
176 (ix) FEATURE:
177 (A) NAME/KEY: CDS
178 (B) LOCATION: 1..387
180 (ix) FEATURE:
181 (A) NAME/KEY: mat_peptide
182 (B) LOCATION: 67..387
185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
187 ATG GAC ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTT CTG CTC TGG      48
188 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
189 -22 -20 -15 -10
191 CTC CCA GGT GCC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCT TCC      96
192 Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
193 -5 -1 1 5 10
195 CTG TCT GCA TCT GTA GGG GAC AGA GTC ACC ATC ACT TGC AGG GCA AGT      144
196 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
197      15      20      25
199 CAG GAC ATT AGG TAT TAT TTA AAT TGG TAT CAG CAG AAA CCA GGA AAA      192
200 Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
201      30      35      40
203 GCT CCT AAG CTC CTG ATC TAT GTT GCA TCC AGT TTG CAA AGT GGG GTC      240
204 Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
205      45      50      55

```

RAW SEQUENCE LISTING DATE: 08/03/2000
 PATENT APPLICATION: US/09/019,441 TIME: 12:07:00

Input Set : A:\012712-502.app
 Output Set: N:\CRF3\08032000\I019441.raw

```

207 CCA TCA AGG TTC AGC GGC AGT GGA TCT GGG ACA GAG TTC ACT CTC ACC      288
208 Pro Ser Arg Phe Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
209      60      65      70
211 GTC AGC AGC CTG CAG CCT GAA GAT TTT GCG ACT TAT TAC TGT CTA CAG      336
212 Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
213 75      80      85      90
215 GTT TAT AGT ACC CCT CGG ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC      384
216 Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
217      95      100      105
219 AAA
220 Lys
224 (2) INFORMATION FOR SEQ ID NO: 4:
226 (i) SEQUENCE CHARACTERISTICS:
227 (A) LENGTH: 411 base pairs
228 (B) TYPE: nucleic acid
229 (C) STRANDEDNESS: single
230 (D) TOPOLOGY: linear
232 (ii) MOLECULE TYPE: DNA (genomic)
235 (ix) FEATURE:
236 (A) NAME/KEY: CDS
237 (B) LOCATION: 1..411
239 (ix) FEATURE:
240 (A) NAME/KEY: mat_peptide
241 (B) LOCATION: 58..411
244 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
246 ATG GAG TTT GGG CTG AGC TGG GTT TTC CTT GTT CCT CTT TTG AAA GGT      48
247 Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly
248 -19      -15      -10      -5
250 GTC CAG TGT GAG GTG CAG CTG GTG GAG TCT GGG GGC GGC TTG GCA AAG      96
251 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
252 -1 1      5      10
254 CCT GGG GGG TCC CTG AGA CTC TGG TGC GCA GCC TCC GGG TTC AGG TTC      144
255 Pro Gly Gly Ser Leu Arg Leu Trp Cys Ala Ala Ser Gly Phe Arg Phe
256 15      20      25
258 ACC TTC AAT AAC TAC TAC ATG GAC TGG GTC CGC CAG GCT CCA GGG CAG      192
259 Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln
260 30      35      40      45
262 GGG CTG GAG TGG GTC TCA CGT ATT AGT AGT GGT GAT CCC ACA TGG      240
263 Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp
264      50      55      60
266 TAC GCA GAC TCC GTG AAG GGC AGA TTC ACC ATC TCC AGA GAG AAC GCC      288
267 Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala
268      65      70      75
270 AAC AAC ACA CTG TTT CTT CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG      336
271 Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
272      80      85      90
274 GCT GTC TAT TAC TGT GCG AGC TTG ACT ACA GGG TCT GAC TCC TGG GGC      384
275 Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly
276      95      100      105

```

RAW SEQUENCE LISTING DATE: 08/03/2000
 PATENT APPLICATION: US/09/019,441 TIME: 12:07:00

Input Set : A:\012712-502.app
 Output Set: N:\CRF3\08032000\I019441.raw

```

278 CAG GGA GTC CTG GTC ACC GTC TCC TCA                411
279 Gln Gly Val Leu Val Thr Val Ser Ser
280 110                115
283 (2) INFORMATION FOR SEQ ID NO: 5:
285     (i) SEQUENCE CHARACTERISTICS:
286         (A) LENGTH: 41 base pairs
287         (B) TYPE: nucleic acid
288         (C) STRANDEDNESS: single
289         (D) TOPOLOGY: linear
291     (ii) MOLECULE TYPE: DNA (genomic)
293     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
295 ATCACAGATC TCTACCATG GACATGAGGG TCCCGCTCA G        41
298 (2) INFORMATION FOR SEQ ID NO: 6:
300     (i) SEQUENCE CHARACTERISTICS:
301         (A) LENGTH: 35 base pairs
302         (B) TYPE: nucleic acid
303         (C) STRANDEDNESS: single
304         (D) TOPOLOGY: linear
306     (ii) MOLECULE TYPE: DNA (genomic)
308     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
310 ATCACAGATC TCTACCATG AGGCTCCCTG CTCAG              35
313 (2) INFORMATION FOR SEQ ID NO: 7:
315     (i) SEQUENCE CHARACTERISTICS:
316         (A) LENGTH: 35 base pairs
317         (B) TYPE: nucleic acid
318         (C) STRANDEDNESS: single
319         (D) TOPOLOGY: linear
321     (ii) MOLECULE TYPE: DNA (genomic)
324     (ix) FEATURE:
325         (A) NAME/KEY: misc_feature
326         (B) LOCATION: 24
327         (D) OTHER INFORMATION: /note= "Nucleotide 24 is N wherein
328 N = A/G."
330     (ix) FEATURE:
331         (A) NAME/KEY: misc_feature
332         (B) LOCATION: 32
333         (D) OTHER INFORMATION: /note= "Nucleotide 32 is N wherein
334 N = T/G."
336     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
338 ATCACAGATC TCTACCATG GAANCCCCAG CNCAG              35
341 (2) INFORMATION FOR SEQ ID NO: 8:
343     (i) SEQUENCE CHARACTERISTICS:
344         (A) LENGTH: 38 base pairs
345         (B) TYPE: nucleic acid
346         (C) STRANDEDNESS: single
347         (D) TOPOLOGY: linear
349     (ii) MOLECULE TYPE: DNA (genomic)
351     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
353 ATCACAGATC TCTACCATG GTGTTGCAGA CCCAGGTC          38

```

VERIFICATION SUMMARY DATE: 08/03/2000
PATENT APPLICATION: US/09/019,441 TIME: 12:07:01

Input Set : A:\012712-502.app
Output Set: N:\CRF3\08032000\I019441.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]